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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 39 Seconds

(Without alignments)
1175.339 Million cell updates/sec

Title: US-09-785-548-2

Perfect score: 1813
Sequence: 1 QMPPSPAPSTIFSGFRHG.....QMOKVLSPLMTMTLVLH 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	344	22	AA667212
2	1802	99.4	610	22	AA667214
3	1802	99.4	610	22	AA667216
4	1656	91.3	319	22	AA641888
5	1648	90.9	319	22	AB111534
6	1646	90.8	313	22	AA604760
7	1645	90.7	313	22	AA640102
8	1640	90.5	313	22	AA667215
9	1640	90.5	313	22	AA667217
10	1234	68.1	363	22	AA687138

Result No.	Score	Query Match	Length	DB ID	Description
11	1234	68.1	363	22	AA019743
12	1234	68.1	363	22	ABP47963
13	573	31.6	811	23	ABG29279
14	567.5	31.3	671	23	AAE17496
15	520.5	28.7	376	22	AA637772
16	520.5	28.7	415	22	AB111731
17	515	28.4	336	22	AAE04779
18	515	28.4	348	22	AA087550
19	515	28.4	348	22	AA019852
20	515	28.4	407	22	AA019725
21	515	28.4	407	23	ABP47945
22	507	28.0	315	22	AA087250
23	507	27.4	708	22	ABE63195
24	497	25.3	550	22	ABE4880
25	459	23.7	234	22	AA087238
26	430.5	23.7	234	22	AA087541
27	430.5	23.7	234	22	AA087541
28	430.5	23.7	234	22	AA087541
29	430.5	23.7	234	22	AA019717
30	430.5	23.7	234	22	ABP47937
31	411.5	22.7	228	21	AA602306
32	346.5	19.1	245	22	AB111754
33	291	16.1	1102	22	ABG29358
34	234.5	12.9	461	22	AA019715
35	234.5	12.9	461	23	ABP47935
36	217	12.0	280	22	ABE59077
37	215.5	11.9	422	17	AA097722
38	213.5	11.8	400	17	AA01114
39	213.5	11.8	400	20	AA083429
40	212.5	11.7	68	22	AA088519
41	212	11.7	412	18	AA025032
42	211.5	11.7	590	23	AB05693
43	211.5	11.7	590	23	AAE17499
44	211.5	11.7	906	23	AB086635
45	209	11.5	405	20	AA027275

ALIGNMENTS

RESULT 1
AA667212
ID AA667212 standard; Protein: 344 AA.
AC AA667212;
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).
XX
KW Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
KW neurodegenerative disease; Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO200160857-A2.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-FR00461.
XX
PR 17-FEB-2000; 2000FR-0001980.
PR 18-APR-2000; 2000US-0198489.
XX
PA (AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Koutnikova H, Brice A, Fournier A, Pradier L, Prades C;
PI Arnaud-Regaigne I, Kosier-Montus M, Corti O;
XX
DR WPI: 2001-550047/61.
XX
N-PSDB: AAH77663.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
 PT interaction partner of Parkin and is useful to treat neurodegenerative
 PT pathologies including Parkinson's disease -

PS Claim 8; Page 58-60; 82pp; French.

CC The present sequence represents a human Parkin-Associated Protein 1
 CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
 CC mutated in certain forms of familial (juvenile autosomal recessive)
 CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
 CC PAP1 is used to treat neurodegenerative diseases, particularly to
 CC diagnose and treat Parkinson's disease.

SQ Sequence 344 AA;

Query Match 100.0%; Score 1813; DB 22; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4,5e-192;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QNLPSPAPSTIFSGFRHGLSIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLEIC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 QNLPSPAPSTIFSGFRHGLSIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLEIC 60

QY 61 IKACKNLAYGEEKKKKKNPYKYTYLLPDRSSQGRKRTGVQRTVDPTQETLKYYQVAPAQ 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 IKACKNLAYGEEKKKKKNPYKYTYLLPDRSSQGRKRTGVQRTVDPTQETLKYYQVAPAQ 120

QY 121 LVTRQLOVSVNHLGTLARVFLGEVITISLATWDFEDSTQSRFMRHLRAKAEKEDSVQ 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LVTRQLOVSVNHLGTLARVFLGEVITISLATWDFEDSTQSRFMRHLRAKAEKEDSVQ 180

QY 181 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGQLCLVILGAKNLPVRPDGTLNSFVK 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGQLCLVILGAKNLPVRPDGTLNSFVK 240

QY 241 CLTLPDQOKLRKSPVLRKQACPOMKHSFVSGVTPAOLROSSLELTWDALEFGMNDRL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CLTLPDQOKLRKSPVLRKQACPOMKHSFVSGVTPAOLROSSLELTWDALEFGMNDRL 300

QY 301 LGGTRLGSGDPTAVGGDACSLSKLOMOKVLSPPNLTMTDTLVILH 344
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LGGTRLGSGDPTAVGGDACSLSKLOMOKVLSPPNLTMTDTLVILH 344

RESULT 2
 AAG67214
 ID AAG67214 standard; Protein: 610 AA.

AAG67214;

DT 13-NOV-2001 (first entry)

XX Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).

DE Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
 KW neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

XX MO200160857-A2.

XX 23-AUG-2001.

PD 15-FEB-2001; 2001WO-FR00461.

PF 17-FEB-2000; 2000FR-0001980.

PR 18-APR-2000; 2000US-0198489.

XX (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Noutchkova H, Brice A, Fournier A, Pradier L, Prades C;
 PI Arnould-Reguigne I, Koster-Montus M, Corti O;

XX NPI: 2001-550047/61.

DR N-PSDB; AAH77672.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
 PT interaction partner of Parkin and is useful to treat neurodegenerative
 PT pathologies including Parkinson's disease -

PS Claim 10; Fig 9; 82pp; French.

CC The present sequence represents a human Parkin-Associated Protein 1
 CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
 CC mutated in certain forms of familial (juvenile autosomal recessive)
 CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
 CC PAP1 is used to treat neurodegenerative diseases, particularly to
 CC diagnose and treat Parkinson's disease.

SQ Sequence 610 AA;

Query Match 99.4%; Score 1802; DB 22; Length 610;
 Best Local Similarity 99.4%; Pred. No. 1.9e-190;
 Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNLPSPAPSTIFSGFRHGLSIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLEIC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 267 QNLPSPAPSTIFSGFRHGLSIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLEIC 326

QY 61 IKACKNLAYGEEKKKKKNPYKYTYLLPDRSSQGRKRTGVQRTVDPTQETLKYYQVAPAQ 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 327 IKACKNLAYGEEKKKKKNPYKYTYLLPDRSSQGRKRTGVQRTVDPTQETLKYYQVAPAQ 386

QY 121 LVTRQLOVSVNHLGTLARVFLGEVITISLATWDFEDSTQSRFMRHLRAKAEKEDSVQ 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 387 LVTRQLOVSVNHLGTLARVFLGEVITISLATWDFEDSTQSRFMRHLRAKAEKEDSVQ 446

QY 181 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGQLCLVILGAKNLPVRPDGTLNSFVK 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 447 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGQLCLVILGAKNLPVRPDGTLNSFVK 506

QY 241 CLTLPDQOKLRKSPVLRKQACPOMKHSFVSGVTPAOLROSSLELTWDALEFGMNDRL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 507 CLTLPDQOKLRKSPVLRKQACPOMKHSFVSGVTPAOLROSSLELTWDALEFGMNDRL 566

QY 301 LGGTRLGSGDPTAVGGDACSLSKLOMOKVLSPPNLTMTDTLVILH 344
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 567 LGGTRLGSGDPTAVGGDACSLSKLOMOKVLSPPNLTMTDTLVILH 610

RESULT 3
 AAG67216
 ID AAG67216 standard; Protein: 610 AA.

AAG67216;

DT 13-NOV-2001 (first entry)

XX Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).

DE Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
 KW neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

XX MO200160857-A2.

XX 23-AUG-2001.

PD 15-FEB-2001; 2001WO-FR00461.

PF 17-FEB-2000; 2000FR-0001980.

PR 18-APR-2000; 2000US-0198489.

XX (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Koutnikova H, Brice A, Fournier A, Pradier L, Prades C;
PI Arnould-Reguigne I, Rosier-Montus M, Corti O;

DR WPI: 2001-550047/61.
DR N-PSDB; AAH77701.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
PT interaction partner of Parkin and is useful to treat neurodegenerative
PT pathologies including Parkinson's disease -

PS Claim 10; Page 77-80; 82pp; French.

CC The present sequence represents a human Parkin-Associated Protein 1
CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
CC mutated in certain forms of familial (juvenile autosomal recessive)
CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
CC PAP1 is used to treat neurodegenerative diseases, particularly to
CC diagnose and treat Parkinson's disease.

CC Sequence 610 AA;

Query Match 99.4%; Score 1802; DB 22; Length 610;
Best Local Similarity 99.4%; Pred. No. 1.9e-190;
Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 QNLPSPAPSTIFSGRHSLSIDSTCTMGFNANNTGELFAHYCFKTHSEIC 60
DB 267 QNLPSPAPSTIFSGRHSLSIDSTCTMGFNANNTGELFAHYCFKTHSEIC 326
QY 61 IKACKNLAYEEKKKKCNPNVKTLYLPDRSSQGRKKTGVONTVDPTFOETLKYVAPAQ 120
DB 327 IKACKNLAYEEKKKKCNPNVKTLYLPDRSSQGRKKTGVONTVDPTFOETLKYVAPAQ 386
QY 121 LVNROLQVSWHGLTLARVFLGEVITSLATWPEDESTOSFRWHPRLAKAEKEDSVQ 180
DB 387 LVNROLQVSWHGLTLARVFLGEVITSLATWPEDESTOSFRWHPRLAKAEKEDSVQ 446
QY 181 SNGELTVRAKLVPSPRKLQEAQEGTDPQSLHGOCLVVLGAKNLPVRPDGTINSFVK 240
DB 447 SNGELTVRAKLVPSPRKLQEAQEGTDPQSLHGOCLVVLGAKNLPVRPDGTINSFVK 506
QY 241 CILTPDQOKRLKSPVLRKQACPQMKHSEVSGVTPAQRLQSSLELTVMQALFGMDRL 300
DB 507 CILTPDQOKRLKSPVLRKQACPQMKHSEVSGVTPAQRLQSSLELTVMQALFGMDRL 566
QY 301 LGSTRGSKGDTAVGSDACSLSLQMKVLSPLMTMTLVH 344
DB 567 LGSTRGSKGDTAVGSDACSLSLQMKVLSPLMTMTLVH 610

```

RESULT 4

AAH41888 standard; Protein: 319 AA.

AAH41888;

22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 6819.

Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokine; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.

Homo sapiens.

MO200153312-AL.

PD 26-JUL-2001.

XX 26-DEC-2000; 2000MO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

PA (HYSE-) HYSEQ INC.

PI Tang Y, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI: 2001-442253/47.

DR N-PSDB; AA161044.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

PS Example 2; SEQ ID NO 6819; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and
the encoded polypeptides (AAH38642-AAH42213) with noctropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

Sequence 319 AA;

Query Match 91.3%; Score 1656; DB 22; Length 319;
Best Local Similarity 99.1%; Pred. No. 1.1e-174;
Matches 313; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 29 CTMGFNANNTGELFAHYCFKTHSEICIKACKNLAYGEEKKKCNPNVKTLYLP 88
DB 4 CTMGFNANNTGELFAHYCFKTHSEICIKACKNLAYGEEKKKCNPNVKTLYLP 63
QY 89 RSSQGRKKTGVONTVDPTFOETLKYVAPAOVLTRQLOVSWHGLTLARVFLGEVIT 148
DB 64 RSSQGRKKTGVONTVDPTFOETLKYVAPAOVLTRQLOVSWHGLTLARVFLGEVIT 123
QY 149 LATWPEDESTOSFRWHPRLAKAEKEDSVPSNGELTVRAKLVPSPRKLQEAQEGTD 208
DB 124 LATWPEDESTOSFRWHPRLAKAEKEDSVPSNGELTVRAKLVPSPRKLQEAQEGTD 183
QY 209 QSLHGOCLVVLGAKNLPVRPDGTINSFVKGCLTLPDQOKRLKSPVLRKQACPQMKH 268
DB 184 QSLHGOCLVVLGAKNLPVRPDGTINSFVKGCLTLPDQOKRLKSPVLRKQACPQMKH 243
QY 269 FVFSGVTPAQRLQSSLELTVMQALFGMDRLGSTRGSKGDTAVGSDACSLQMKVLS 328
DB 244 FVFSGVTPAQRLQSSLELTVMQALFGMDRLGSTRGSKGDTAVGSDACSLQMKVLS 303
QY 329 VLSSPRLMTMTLVH 344
DB 304 VLSSPRLMTMTLVH 319

```

RESULT 5
 ABB11534
 ID ABB11534 standard; peptide: 319 AA.
 AC ABB11534:
 DT 11-JAN-2002 (first entry)
 XX
 XX Human granulophilin-a homologue, SEQ ID NO:1904.
 DE
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KW cystostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vinegary; antilucer.
 XX
 XX Homo sapiens.
 OS
 PN MO200157188-A2.
 PD 09-AUG-2001.
 PF 05-FEB-2001; 2001MO-US03800.
 PR 03-FEB-2000; 2000US-046914.
 XX 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI: 2001-457740/49.
 DR N-PSDB; ABA08778.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 CC
 CC Claim 20; Page 209; 1963pp; English.
 CC
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,

arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 CC
 XX
 XX Sequence 319 AA:
 SQ
 Query Match 90.9%; Score 1648; DR 22; Length 319;
 Best Local Similarity 98.7%; Pred. No. 8,1e-174;
 Matches 312; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 29 CTEMGNFNANTGTEIPAIHYCFKTHSLKICAKKNLAYGEEKKKCNPKYKTYLLPD 88
 DB 4 CTEMGNFNANTGTEIPAIHYCFKTHSLKICAKKNLAYGEEKKKCNPKYKTYLLPD 63
 QY 89 RSSQGRKRTGVQRMVDPPTFQETLKYQVAPQALVTQLOYSVNHGLTLARVFLGEVIT 148
 DB 64 RSSQGRKRTGVQRMVDPPTFQETLKYQVAPQALVTQLOYSVNHGLTLARVFLGEVIT 123
 QY 149 LATWDFEDSTQSFRRHPIRAKAEKEDSVPOSGELTVRAKLVLSRPRLKLEDAEGTD 208
 DB 124 LATWDFEDSTQSFRRHPIRAKADKEDSVPOSGELTVRAKLVLSRTKRLQDAEGTD 183
 QY 209 QPSLHGQLCLVVLGAKNLPYRDPGLTNSFYKGCGLTLPDQOKLRLKSVYLKKACPOWKHS 268
 DB 184 QPSLHGQLCLVVLGAKNLPYRDPGLTNSFYKGCGLTLPDQOKLRLKSVYLKKACPOWKHS 243
 QY 269 FVPSGYTPAQRLRSSLELTYWQDALFGMDRLLGFTLGSKSGPTAVGDCSLSKLOMOK 328
 DB 244 FVPSGYTPAQRLRSSLELTYWQDALFGMDRLLGFTLGSKSGPTAVGDCSLSKLOMOK 303
 QY 329 VLSPPNMLTMDTLVLH 344
 DB 304 VLSPPNMLTMDTLVLH 319
 DE
 XX
 XX Human vesicle trafficking protein-3 (VETRP-3) protein.
 KW Human; vesicle trafficking protein-3; VETRP-3; vaccine; cystic fibrosis;
 KW glucose-galactose malabsorption syndrome; hypercholesterolaemia; goitre;
 KW diabetes mellitus; diabetes insipidus; hyperglycaemia; hypoglycaemia;
 KW Grave's disease; Cushing's disease; Addison's disease; AIDS; allergy;
 KW ulcerative colitis; gastrointestinal disorder; asthma; hay fever; gout;
 KW autoimmune disease; inflammatory disease; bowel disease; osteoporosis;
 KW multiple sclerosis; rheumatoid arthritis; psoriasis; anaemia; cancer;
 KW pancreatitis; Crohn's disease; glomerulonephritis; atherosclerosis;
 KW Goodpasture's syndrome; Hashimoto's thyroiditis; gene therapy; virucide;
 KW systemic lupus erythematosus; dermatitis; nephrotropic; antihelminthic;
 KW cerebroprotective.
 KW
 KW Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 11..128
 FT Domain /note="C2 domain"

FT Domain 13..69 /note= "Protein kinase C C2 domain"
 FT Domain 26..115 /note= "Protein kinase C C2 domain"
 FT Domain 54..79 /note= "C2 domain motif"
 FT Domain 185..273 /note= "Protein kinase C C2 domain"
 FT Domain /note= "Protein kinase C C2 domain"
 PN WO200146256-A2.
 PD 28-JUN-2001.
 XX 21-DEC-2000; 2000WO-US34919.
 XX 21-DEC-1999; 99US-0172968.
 XX 23-DEC-1999; 99US-0172066.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Tang YT, Yue H, Bandman O, Hillman JL, Baughn MR, Lu DAM;
 DR Azimzai Y, Yang J, Burford N, Au-Young J, Reddy R;
 DR MPI: 2001-418040/44.
 DR N-PSDB; AAD09373.
 XX Novel human vesicle trafficking proteins useful for treating and
 PT preventing vesicle trafficking disorders, autoimmune/inflammatory
 PT disorders and cancers -
 PS Claim 1; Page 103; 14pp; English.
 XX The present sequence is human vesicle trafficking protein-3 (VETRP-3)
 CC or protein VETRP-3 is used as vaccine. VETRP-3 is useful for treating a disease
 CC or condition associated with decreased expression of functional VETRP-3
 CC such as vesicle trafficking disorders e.g., cystic fibrosis, glucose-
 CC galactose malabsorption syndrome, hypercholesterolaemia, diabetes
 CC mellitus, diabetes insipidus, hyperglycaemia, hypoglycaemia, Grave's
 CC disease, goitre, Cushing's disease, Addison's disease, gastrointestinal
 CC disorders including ulcerative colitis, AIDS, allergies including
 CC asthma, hay fever, autoimmune/inflammatory diseases including
 CC inflammatory bowel disease, multiple sclerosis, rheumatoid arthritis,
 CC osteoporosis, viral, bacterial, fungal, helminthic and protozoal
 CC infections, psoriasis, pancreatitis, anaemia, Crohn's disease,
 CC glomerulonephritis, atherosclerosis, dermatitis, Hashimoto's
 CC thyroiditis, gout, Goodpasture's syndrome, systemic lupus erythematosus
 CC and cancers. VETRP polynucleotides are useful in gene therapy and
 CC diagnostic purposes.
 CC Sequence 313 AA;
 Query Match 90.8%; Score 1646; DB 22; Length 313;
 Best Local Similarity 99.7%; Pred. No. 1.3e-173;
 Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 312 ADGWS

Db 241 SGVTPAQLROSSLELTWVQALFGMNDRLIGTRLSKGDPTAVGAGDACSLSKLQWOKVLS 300
 QY 332 SPNLWTMDTLVLH 344
 Db 301 SPNLWTMDTLVLH 313
 RESULT 7
 AAM40102
 ID AAM40102 standard; Protein; 313 AA.
 XX AAM40102;
 XX 22-OCT-2001 (first entry)
 DT Human polypeptide SEQ ID NO 3247.
 DE Human polypeptide SEQ ID NO 3247.
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukaemia.
 XX Homo sapiens.
 OS
 XX WO200153312-A1.
 PN 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 PF 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou F, Goodrich R, Drmanac RT;
 XX MPI: 2001-442253/47.
 DR N-PSDB; AAI59258.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PT Example 5; SEQ ID NO 3247; 10078pp; English.
 XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC Sequence 313 AA;
 SQ

Query Match	90.7%	Score 1645;	DB 22;	Length 313;
Best Local Similarity	99.7%	Pred. No. 1.7e-173;		
Matches 312; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	32	MGNEDNANTGIEFAIHAYCEFTHSLEICINACKNLATAGEKKKCNVYKTYLLPDBSS	91
Db	1	MGNEDNANTGIEFAIHAYCEFTHSLEICINACKNLATAGEKKKCNVYKTYLLPDBSS	60
QY	92	QKKRRTGVRNTVPDTPBEDTLKYQVAPQALYTRQLOVSVMHLGTLARVFLGEVILSIAT	15
Db	61	QKKRRTGVRNTVPDTPBEDTLKYQVAPQALYTRQLOVSVMHLGTLARVFLGEVILSIAT	124
QY	152	WDFEDSTQSFRRWHPRLRKAKEKYEDSVQSGNELTVRAKVLPSRPRKLOEAOGSTOPS	21
Db	121	WDFEDSTQSFRRWHPRLRKAKEKYEDSVQSGNELTVRAKVLPSRPRKLOEAOGSTOPS	187
QY	212	LHGOLCLVYLGAKNLVPAPBDTILNSFYKGCITLDPQOKLRLKSPVLRKQACPQWKHSFV	277
	181	LHGOLCLVYLGAKNLVPAPBDTILNSFYKGCITLDPQOKLRLKSPVLRKQACPQWKHSFV	240
QY	272	SGVTPAOLROSSELTFWQDALFGMNRRLGGTRIGSGDPAVAGDACSUSKLOMOKVLS	333
Db	241	SGVTPAOLROSSELTFWQDALFGMNRRLGGTRIGSGDPAVAGDACSUSKLOMOKVLS	300
QY	332	SPNLATDMTLVLH 344	
Db	301	SPNLATDMTLVLH 313	

RESULT 8
AAG67215
ID AAG67215 standard; Protein; 313 AA
yy

AC	AAG67215;
XX	
DT	13-NOV-2061 (first entry)
XX	

Amino acid sequence of human Parkin-Associated Protein 1 (PAP1)

KW Human; Parkin-Associated Protein 1; PAP1; Parkin gene
 KW neurodegenerative disease; Parkinson's disease.
 XX
 Homo sapiens.
 OS

Homo sapiens.

PN W0200160857-A2

23-AUG-2001

15-FEB-2001; 2001WO-FR00461.

PR 17-FEB-2000; 2000FR-0001980;
PR 18-APR-2000; 2000US-0198489.

PR 18-APR-2000; 2000US-0198489.

PA (AVET) AVENTIS PHARMA SA,
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE

PI Koutnikova H, Brice A, Fournier A, Pradier L, Prades C
PI Arnould-Reguinne I, Rosier-Montus M, Corti O;

DR WPI; 2001-550047/61.
DR N-PSDB; AAH77673.

DR N-PSDB; AAH77673

pathologies including Parkinson's disease - to treat neurodegenerative

PS Claim 10; Fig 10; 82pp; French

The present sequence represents a human Parkin-Associated Protein 1 (PAP1) protein. PAP1 is associated with the parkin gene, which is 'mutated in certain forms of familial (juvenile autosomal recessive) Parkinson's disease. PAP1 has some homology with synaptotagmins.

CC PAPI1 is used to treat neurodegenerative diseases, particularly to
CC diagnose and treat Parkinson's disease.
XX
SQ Sequence 313 AA;

Sequence 313 AA,

Query Match	90.5%	Score 1640:	DB 22:	Length 313;
Best Local Similarity	99.4%;	Pred. No. 6.1e-173;		
Matches 31;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

QY	32	MGNNDNANVGEIEFAIHCHYCKHTSLEICIAACNNLWAGEBKKKCNBPYVTTYLLPBRSS	91
Db	1	MGNEDNANVNTGEIEFALHCHYCKHTSLEICIAACNNLWAGEBKKKCNBPYKTYLLPBRSS	60
QY	92	QGRKRTVQRTVPTPTQOETLKYVAAQAOLVTRLOLYSVWHGLGTLARVLEGVEVYISLAT	151
Db	61	QGRKRTVQRTVPTPTQOETLKYVAAQAOLVTRLOLYSVWHGLGTLARVLEGVEVYIIPLAT	120
QY	152	WDFEDSTTQSFRRMHPRLAKAEKYEDSVPOSNGELTVRAKLVLPSPRPRLQDAOGSTQPS	211
Db	121	WDFEDSTTQSFRRMHPRLAKAEKYEDSVPOSNGELTVRAKLVLPSPRPRLQDAOGSTQPS	180
QY	212	LHGGLCLVYLGANLPLVRPBGTLNSFPKGCGLTLPDOOKRLKSPVLRKQACPOWKHSFVF	277
Db	181	LHGGLCLVYLGANLPLVRPBGTLNSFPKGCGLTLPDOOKRLKSPVLRKQACPOWKHSFVF	240
QY	272	SGVTPAOLROSSLELTIVWDALFGMNDRLGLGTRLSGSGTAVGADGACSAKLOMOKVLS	331
Db	241	SGVTPAOLROSSLELTIVWDALFGMNDRLGLGTRLSGSGTAVGADGACSAKLOMOKVLS	300
QY	332	SPNLMTDMTLYLH 344	
Db	301	SPNLMTDMTLYLH 313	

RESULT 9
AAG67217
ID AAG67217 standard; Protein; 313 AA
yy

AC AAG67217;
XY

DT 13-NOV-2001 (first entry)
XX

Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).

Human; Parkin-Associated Protein 1; PAPI; parkin gene neurodegenerative disease; Parkinson's disease.

05 Homo sapiens
XX

PN WO200160857-A2
XX

PD 23-AUG-2001
XX

15-FEB-2001; 2001WO-FR00461

17-FEB-2000; 2000FR-0001980
18-APR-2000: 2000TS-0198489

17-FEB-2000; 2000FR-0001980
18-APR-2000: 2000TS-0198489

PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST SANTE & RECH MEDICALE
X

Arnould-Reguigne I, Rosier-Montus M, Corti O; Prades C

WPL: 2001-550041/61
N-PSDB: AAH77702

WFL; 2001-550041/
N-PSDB: AAH77702

A new protein, designated Parkin-Associated Protein 1 (PAP1), is an interaction partner of Parkin and is useful to treat neurodegenerative pathologies including Parkinson's disease -

Claim 10; Page 80-82; 82pp; French

CC The present sequence represents a human Parkin-associated Protein 1
CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
CC mutated in certain forms of familial (juvenile autosomal recessive)
CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
CC PAP1 is used to treat neurodegenerative diseases, particularly to
CC diagnose and treat Parkinson's disease.

XX Sequence 313 AA:

Query Match 90.5%; Score 1640; DB 22; Length 313;

Best Local Similarity 99.4%; Pred. No. 6, 1e-173;

Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 MGNFNNVNTGEIEFAIHYCFKTHSLEICIKACKNLAYGEEKKKCNPYKYTLPPDRSS 91
DB 1 MGNFNNVNTGEIEFAIHYCFKTHSLEICIKACKNLAYGEEKKKCNPYKYTLPPDRSS 60
QY 92 QGKRRGTGVRNVDPRFOETLKQVAPADLVTRQLOVSWHGLTARVVLGVIISLAT 151
DB 61 QGKRRGTGVRNVDPRFOETLKQVAPADLVTRQLOVSWHGLTARVVLGVIISLAT 120
DB 152 WDFEDSTTOSFPMHPLRAKAEKEDSVPSNGELTVRAKLVLPSRPRLQEOEGTDOPS 211
DB 121 WDFEDSTTOSFPMHPLRAKAEKEDSVPSNGELTVRAKLVLPSRPRLQEOEGTDOPS 180
QY 212 LHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQKLRKSPVLKQACPOMKHSFVF 271
DB 181 LHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQKLRKSPVLKQACPOMKHSFVF 240
QY 272 SGVTYPAQLRSSLELTVMOQALFGMDRLTGTRLSKSGPTAVGACASLSKLOMOKVLS 331
DB 241 SGVTYPAQLRSSLELTVMOQALFGMDRLTGTRLSKSGPTAVGACASLSKLOMOKVLS 300
QY 332 SPNLWTMDTLVLH 344
DB 301 SPNLWTMDTLVLH 313

RESULT 10
ID AAU87138 standard; Protein; 363 AA.
AAU87138
AC AAU87138;
XX 05-JUN-2002 (first entry)
DE Novel central nervous system protein #48.
XX
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
XX nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
XX acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
XX adenocarcinoma; reproductive system disorder; testicular feminisation;
XX endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
XX respiratory disorder; renal disorder; kidney failure; blood disorder;
XX myocardial infarction; wound healing; cell proliferation; skin aging;
XX food additive; food preservative; gene therapy.
OS Homo sapiens.
XX
XX WO200155318-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01332.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0228927.
PR 01-SEP-2000; 2000US-0228343.
PR 01-SEP-2000; 2000US-0228344.
PR 01-SEP-2000; 2000US-0228345.
PR 05-SEP-2000; 2000US-0228509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0234201.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235834.
PR 26-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0235837.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.

Query Match	68.1%	Score 1234	DB 22	Length 363	
Best Local Similarity	97.5%	Pred. No. 8.9e-128			
Matches 234	Conservative	0	Mismatches 6	Indels 0	Gaps 0
Oy	1	QNLPSAPSPSTFSGCFHSHLSIDSTCTEKGNDNANVTGEIEFAHYCFKTSLEIC	60		
Db	124	QNLPSAPSPSTFSGCFHSHLSIDSTCTEKGNDNANVTGEIEFAHYCFKTSLEIC	183		
Oy	61	IKACKNLAYGEBKKKKCNPKYKTYLLPPRSSGKKRTGVORNTYDPTFOEFLKYTAPAQ	120		
Db	184	IKACKNLAYGEBKKKKCNPKYKTYLLPPRSSGKKRTGVORNTYDPTFOEFLKYTAPAQ	243		
Oy	121	LVTRQLQSVNHLGLTARVFEGLVYIISLAWDFEDSTQTSFRRMHLPAKAKEXEDSPQ	180		
Db	244	LVTRQLQSVNHLGLTARVFEGLVYIISLAWDFEDSTQTSFRRMHLPAKAKEXEDSPQ	303		
Oy	181	SNGELTVAKLVLPSPRKKLOADEGDTQPSLRGQLCLVYTGAKNLPVRPDGTLNSFYKG	240		
Db	304	SNGELTVAKLVLPSPRKKLOADEGDTQPSLRGQLCLVYTGAKNLPVRPDGTLNSFYKG	363		
RESULT 11					
ID	AAU19743				
ID	AAU19743	standard; Protein; 363 AA.			
XX	AAU19743;				
AC					
XX					
DT	06-DEC-2001	(first entry)			
XX					
DE	Human novel extracellular matrix protein, Seg ID No 393.				
XX					
KW	Human; secreted extracellular matrix protein; immunomodulatory;				
KW	Anti-HIV; antihaemic; antirheumatic; antileukemic; cardiatic; vascular;				
KW	cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytosaric;				
KW	antialzheimers; immune/autoimmune disease; HIV infection; anaemia;				
KW	human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;				
KW	cancers; hyperproliferative disorder; Breast neoplasia; melanoma;				
KW	Alzheimer syndrome; Gaucher's disease; neurological diseases;				
KW	Sezary's disease; Parkinson's disease; cardiovascular disorder;				
KW	cardiac arrest; tachycardia; angina; infection; corneal infections;				
KW	wound healing; immunogen; gene therapy; antisense; food additive.				
XX					
OS	Homo sapiens.				
XX					
PN	W0200155368-A1.				
XX					
PD	02-AUG-2001.				
XX					
PF	17-JAN-2001; 2001WO-US01348.				
XX					
RR	31-JAN-2000; 2000US-0179065.				

PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226688.
 PR 22-AUG-2000; 2000US-0227009.
 PR 23-AUG-2000; 2000US-0227009.
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 PR 01-SEP-2000; 2000US-0229287.
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 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
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 PR 08-SEP-2000; 2000US-0231413.
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 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
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 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241721.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
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 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
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 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251038.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001:465572/50.
 N-PSDB; AAS31314.

Nucleic acid molecules encoding human secreted extracellular matrix
 proteins, used in preventing, treating or ameliorating a disorder, e.g.
 Alzheimer's and Parkinson's diseases and cancers -

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html?poocid=999909764870.

XX Sequence 363 AA;

Query Match 68.1%; Score 1234; DB 23; Length 363;
 Best Local Similarity 97.5%; Pred. No. 8.9e-128;
 Matches 234; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 QNLSSPAPSTIFSGFRHGLISIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLETC 60
 124 QNLSSPAPSTIFSGFRHGLISIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLETC 183

QY 61 IKACKNLAYGEEKKKCKMPYKTYLLPDRSSGKKRTGVORNTVDPFQETLKYQVAPAQ 120
 DB 184 IKACKNLAYGEEKKKCKMPYKTYLLPDRSSGKKRTGVORNTVDPFQETLKYQVAPAQ 243

QY 121 LVTRQLOYSVHMLGTLARVFLGEVYIISLATWDFEDSTTQSFRRHPLRAKAEKYEDSVPO 180
 DB 244 LVTRQLOYSVHMLGTLARVFLGEVYIISLATWDFEDSTTQSFRRHPLRAKAEKYEDSVPO 303

QY 181 SNGELTVAKILVPSRPKRLQEAOGSTDPQLHGQLCLVYLGAKNLPVPRDGLNSFVKG 240
 DB 304 SNGELTVAKILVPSRPKRLQEAOGSTDPQLHGQLCLVYLGAKNLPVPRDGLNSFVKG 363

RESULT 13

ABG29279 standard; Protein: 811 AA.

XX AC ABG29279;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #29270.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX MO200175067-A2.

XX PD 11-OCT-2001.

XX PE 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI: 2001-639362/73.

XX DR N-PSDB: AAS93466.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PT
 PS Claim 20; SEQ ID NO 59638; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 811 AA;

Query Match 31.6%; Score 573; DB 22; Length 811;
 Best Local Similarity 39.2%; Pred. No. 7.4e-54;
 Matches 136; Conservative 57; Mismatches 132; Indels 22; Gaps 8;

QY 14 SSGFRHGLISIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLETCIKACKNLAYGEEK 73
 DB 363 ASGISTSLNSMMSVYSTGYGNKVSCEILLHSYCKTGGTLTFKACNLAIQDCK 422

QY 74 KKKCNPYKTYLLPDRSSGKKRTGVORNTVDPFQETLKYQVAPOLVTRQLOYSVHML 133
 DB 423 KQRTDAYVYSYLLPDKSNMNRKRTKIRGTG-NPEFENETLKYTISHTQETTRQLQSVHMX 481

QY 134 GTLARKVFLGEVYIISLATWDFEDSTTQSFRRHPLRAKAEKYDSVPQSGELTVAKILV 193
 DB 482 DRFGNSFLGEVEIPIFDSMNPEPTDE--WFLQPKVEFADIDQLQYKGETLVLYLRYP 538

QY 194 PSR-----PRKLO-----EAQEGTDQPSLHGQLCLV-VILGAKNL-PVPRDGLNSFVKG 241
 DB 539 PEENMLPPEQLOGNKTKTKKKKSPVYISGILEVFTKEAKNLPAVKSGETSDSVKRY 598

QY 242 LTPDQOKLRLKSPVLRQACPQWKHSFVSGVTPPAOLROSSLELTVDQALFGMNDRL 301
 DB 599 LTPDQOKLRLKSPVLRQACPQWKHSFVSGVTPPAOLROSSLELTVDQALFGMNDRL 657

QY 302 GGTRLGSKGTAVAG-----DACSLSKLOKQVLSSPNLMTMTLYL 343
 DB 658 GGTRLGSKGTAVAG-----DACSLSKLOKQVLSSPNLMTMTLYL 704

RESULT 14

AAE17496 standard; Protein: 671 AA.

XX AC AAE17496;

XX DT 22-APR-2002 (first entry)

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

XX DE Human secretion and trafficking protein-5 (SAT-5).

Human; secretion and trafficking protein-5; vesicle trafficking disorder;
 KW SAT-5; cystic fibrosis; diabetes mellitus; gastrointestinal disorder;
 KW Grave's disease; ulcerative colitis; cardiac disorder; hypertension;
 KW polyostitis; neurological disorder; Alzheimer's disease; dementia;
 KW depression; epilepsy; Tourette's disorder; cell proliferative disorder;
 KW cirrhosis; cancer; autoimmune disorder; inflammatory disorder; AIDS;
 KW acquired immune deficiency syndrome; Addison's disease; allergy; asthma;
 KW atherosclerosis; sickle cell anaemia; hyperglycaemia; transgenic animal;
 KW gene therapy; hypotensive; nootropic; neuroprotective; antidepressant;

Db 115 CKNLAYGEEKKKCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQGLMT 174
 QY 124 ROLQSVNHLGTLARVFLGEVYIISLATWDFEDSTQSRMHMLRAKAEYEDSVQSNQ 183
 Db 175 RRLQSVNHLGTLARVFLGEVYIISLATWDFEDSTQSRMHMLRAKAEYEDSVQSNQ 234
 QY 184 ELTVRAKLVLSRPRLQEAOGTDPRLHGLCLVVLGAKNLPVPRDGLNSFVAGCLT 243
 Db 235 ELAVRAKLVLPAGPRKPEADQEG--QLALNGQLCLVVLGAKNLPVPRDGLNSFVAGCLT 292
 QY 244 LPDOOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 303
 Db 293 LPNOOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 352
 QY 304 TRLGSGDPTAVGDAACSLKLOMOKVLSSPNLMTMTLVH 344
 Db 353 ARLGSKGAACGCPDGSQSKLOMOKVLSSPNLMTMTLVH 393

Query Match 81.1%; Score 1471; DB 11; Length 393;
 Best Local Similarity 81.8%; Pred. No. 4, 7e-131;
 Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;

AC 099N48 PRELIMINARY; PRT; 393 AA.
 ID 099N48
 AC 099N48; 01-JUN-2001 (Tremblrel, 17, Created)
 DT 01-JUN-2001 (Tremblrel, 17, last sequence update)
 DT 01-JUN-2001 (Tremblrel, 19, last annotation update)
 DE Synaptotagmin-like protein 3-a delta 35-II.
 GN SYTL3 OR SLP3-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=21226169; PubMed=11327731;
 RA Fukuda M., Saegusa C., Mikoshiba K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain";
 RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL; AB057765; BAB41093.1; -;
 DR MGD; MGI:1933367; SYTL3.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS50004; C2_DOMAIN_2; 2.
 SQ SEQUENCE 393 AA; 43755 MW; D6D27768F455F91B CRC64;

Query Match 81.1%; Score 1471; DB 11; Length 393;
 Best Local Similarity 81.8%; Pred. No. 4, 7e-131;
 Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;
 QY 4 PSSPAPSTFFSGGFRHSLISIDSTCTEMGNFNDNAVNTGEIEFAIHCFKTHSLCICIK 63
 Db 55 PSSPAPSTFFSGGFRHSLISIDSTCTEMGNFNDNAVNTGEIEFAIHCFKTHSLCICIK 114
 QY 64 CKNLAYGEEKKKCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQGLMT 123
 Db 115 CKNLAYGEEKKKCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQGLMT 174
 QY 124 ROLQSVNHLGTLARVFLGEVYIISLATWDFEDSTQSRMHMLRAKAEYEDSVQSNQ 183
 Db 175 ROLQSVNHLGTLARVFLGEVYIISLATWDFEDSTQSRMHMLRAKAEYEDSVQSNQ 234
 QY 184 ELTVRAKLVLSRPRLQEAOGTDPRLHGLCLVVLGAKNLPVPRDGLNSFVAGCLT 243
 Db 235 ELAVRAKLVLPAGPRKPEADQEG--QLALNGQLCLVVLGAKNLPVPRDGLNSFVAGCLT 292
 QY 244 LPDOOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 303
 Db 293 LPNOOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 352
 QY 304 TRLGSGDPTAVGDAACSLKLOMOKVLSSPNLMTMTLVH 344

Db 353 ARLGSKGAACGCPDGSQSKLOMOKVLSSPNLMTMTLVH 393

RESULT 3

QY 099N49 PRELIMINARY; PRT; 412 AA.
 ID 099N49
 AC 099N49; 01-JUN-2001 (Tremblrel, 17, Created)
 DT 01-JUN-2001 (Tremblrel, 17, last sequence update)
 DT 01-JUN-2002 (Tremblrel, 21, last annotation update)
 DE Synaptotagmin-like protein 3-a + 35-I (Synaptotagmin-like 3).
 GN SYTL3 OR SLP3-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=21226169; PubMed=11327731;
 RA Fukuda M., Saegusa C., Mikoshiba K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain";
 RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL; BC022608; AAB22608.1; -;
 DR MGD; MGI:1933367; SYTL3.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS50004; C2_DOMAIN_2; 2.
 SQ SEQUENCE 412 AA; 45954 MW; AB1EDD538CCCB218 CRC64;

Query Match 81.1%; Score 1471; DB 11; Length 412;
 Best Local Similarity 81.8%; Pred. No. 5e-131;
 Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;

QY 4 PSSPAPSTFFSGGFRHSLISIDSTCTEMGNFNDNAVNTGEIEFAIHCFKTHSLCICIK 63
 Db 74 PSSPAPSTFFSGGFRHSLISIDSTCTEMGNFNDNAVNTGEIEFAIHCFKTHSLCICIK 133
 QY 64 CKNLAYGEEKKKCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQGLMT 123
 Db 134 CKNLAYGEEKKKCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQGLMT 193
 QY 124 ROLQSVNHLGTLARVFLGEVYIISLATWDFEDSTQSRMHMLRAKAEYEDSVQSNQ 183
 Db 194 ROLQSVNHLGTLARVFLGEVYIISLATWDFEDSTQSRMHMLRAKAEYEDSVQSNQ 253
 QY 184 ELTVRAKLVLSRPRLQEAOGTDPRLHGLCLVVLGAKNLPVPRDGLNSFVAGCLT 243
 Db 254 ELAVRAKLVLPAGPRKPEADQEG--QLALNGQLCLVVLGAKNLPVPRDGLNSFVAGCLT 311
 QY 244 LPDOOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 303
 Db 312 LPNOOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 371
 QY 304 TRLGSGDPTAVGDAACSLKLOMOKVLSSPNLMTMTLVH 344
 Db 372 ARLGSKGAACGCPDGSQSKLOMOKVLSSPNLMTMTLVH 412

RESULT 4
 QY 099N54 PRELIMINARY; PRT; 607 AA.
 ID 099N54
 AC 099N54; 01-JUN-2001 (Tremblrel, 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Synaptotagmin-like protein 3-a.
 GN SYTL3 OR SLP3-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE-21226169; PubMed-11327731;
 RA Fukuda M., Saegusa C., Mikoshida K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain".
 RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL; AB057758; BAB41086.1; -;
 DR MGD; MGI:1933367; SYTL3.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR SMART; SM00239; C2; 2.
 PROSITE; PS50004; C2_DOMAIN_2; 2.
 SEQUENCE 607 AA; 68567 MW; F9F404D2D77A6351 CRC64;
 Query Match 81.1%; Score 1471; DB 11; Length 607;
 Best Local Similarity 81.8%; Pred. No. 8.7e-131;
 Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;
 QY 4 PSSPASTFSGGFRHGLISIDSTCTEMGNFDNANVTGEIEFAHYCEKTHSEICIK 63
 DB 269 PSSPTSAFVSGGLRHGSLISINSTEEMGNFDNANVTGEIEFAHYCEKTHSEICIK 328
 QY 64 CNLAAGEEKKKCNPKYKYLPPDRSSQGRKRTGVARNVPTFOETLKQVAPAOGLVT 123
 DB 329 CNLAAGEEKKKCNPKYKYLPPDRSSQGRKRTGVARNVPTFOETLKQVAPAOGLVT 388
 QY 124 ROLQVSVHMLGTARVFLGCVISLATWDFEDSTQSFRRHPLRAKEKEDSVPOSNG 183
 DB 389 RLQVSVHMLGTARVFLGCVISLATWDFEDSTQSFRRHPLRAKEKEDSVPOSNG 448
 QY 184 ELTVRAKLVLPSPRRKLQEAQEGTDQPSLHGOLCLVYLGAKNLPVRPDGTLNFEVGGLT 243
 DB 449 ELTVRAKLVLPSPRRKLQEAQEGTDQPSLHGOLCLVYLGAKNLPVRPDGTLNFEVGGLT 506
 QY 244 LPDQQLRLKSPYLKQACPOKHSFVPSVTPAQLKQSSLELTWVQALFGMNDRLIGE 303
 DB 507 LPDQQLRLKSPYLKQACPOKHSFVPSVTPAQLKQSSLELTWVQALFGMNDRLIGE 566
 QY 304 TRLSKGDVAVGDACTSLKLOKQVILSSPNLMTDMLVLH 344
 DB 567 ARLGSKGAAGCPDSGSQSKLOMHRVILSSPNLMTDMLVLH 607
 RESULT 5
 Q99N47 PRELIMINARY; PRT; 311 AA.
 AC 099N47;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Synaptotagmin-like protein 3-b + 3S-III.
 GN SYTL3 OR SLP3-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE-21226169; PubMed-11327731;
 RA Fukuda M., Saegusa C., Mikoshida K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain".

RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL; AB057758; BAB41094.1; -;
 DR MGD; MGI:1933367; SYTL3.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR SMART; SM00239; C2; 2.
 PROSITE; PS50004; C2_DOMAIN_2; 2.
 SEQUENCE 311 AA; 34884 MW; 91986B928DC510E0 CRC64;
 Query Match 74.7%; Score 1354; DB 11; Length 311;
 Best Local Similarity 82.1%; Pred. No. 4.2e-120;
 Matches 257; Conservative 28; Mismatches 26; Indels 2; Gaps 1;
 QY 32 MGNFDNANVTGEIEFAHYCEKTHSEICIKACKNLAAGEEKKKCNPKYKYLPPRSS 91
 DB 1 MGNFDNANVTGEIEFAHYCEKTHSEICIKACKNLAAGEEKKKCNPKYKYLPPRSS 60
 QY 92 QGRKRTGVARNVPTFOETLKQVAPAOGLVTROLOVSVHMLGTARVFLGCVISLAT 151
 DB 61 QGRKRTGVARNVPTFOETLKQVAPAOGLVTROLOVSVHMLGTARVFLGCVISLAT 120
 QY 152 WDFEDSTQSFRRHPLRAKEKEDSVPOSNGELTVRAKLVLPSPRRKLQEAQEGTDQPS 211
 DB 121 WDFEDSTQSFRRHPLRAKEKEDSVPOSNGELTVRAKLVLPSPRRKLQEAQEGTDQPS 178
 QY 212 LFGOLCLVYLGAKNLPVRPDGTLNFEVGGLTLPDQQLRLKSPYLKQACPOKHSFVF 271
 DB 179 LFGOLCLVYLGAKNLPVRPDGTLNFEVGGLTLPDQQLRLKSPYLKQACPOKHSFVF 238
 QY 272 SCVTPAQLKQSSLELTWVQALFGMNDRLIGTRLSKGDVAVGDACTSLKLOKQVILSS 331
 DB 239 NGVSSQLKQSSLELTWVQALFGMNDRLIGTRLSKGDVAVGDACTSLKLOKQVILSS 298
 QY 332 SPNLMTDMLVLH 344
 DB 299 SPNLMTDMLVLH 311
 RESULT 6
 Q9TDM5 PRELIMINARY; PRT; 730 AA.
 AC 09TDM5;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Synaptotagmin-like protein 5.
 GN SLP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Kuroda T.S., Fukuda M., Ariga H., Mikoshida K.;
 RT "Synaptotagmin-like protein 5: A novel Rab27A effector with C-terminal
 tandem C2 domains".
 RL Biochem. Biophys. Res. Commun. 0:0-0(2002).
 DR EMBL; AB080222; BAB88906.1; -;
 PROSITE; PS50004; D9E0DA98880A95ED CRC64;
 SEQUENCE 730 AA; 81522 MW; D9E0DA98880A95ED CRC64;
 Query Match 31.6%; Score 573; DB 4; Length 730;
 Best Local Similarity 39.2%; Pred. No. 1.8e-45;
 Matches 136; Conservative 57; Mismatches 132; Indels 22; Gaps 8;
 QY 14 SGGFRHGLISIDSTCTEMGNFDNANVTGEIEFAHYCEKTHSEICIKACKNLAAGEEK 73
 DB 380 ASGLSTSLNMSVSVSETGDYGNKVSCEILHISYCYKGTGLTFVKNCRMLATGDEK 439
 QY 74 KKKCNPKYKYLPPDRSSQGRKRTGVARNVPTFOETLKQVAPAOGLVTROLOVSVHML 133
 DB 440 KORDAVYKSYLLPDKSRNKKRTKIRGT-NPEFETLKYSHTQLETRTLQSLVSHYH 498


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RESULT 10
GRAB07
08VH07 PRELIMINARY; PRT; 672 AA.
08VH07;
01-MAR-2002 (TREMBLrel_20, Created)
01-MAR-2002 (TREMBLrel_20, Last sequence update)
01-JUN-2002 (TREMBLrel_21, Last annotation update)
GRanuph1lin A.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
Rat Copola T., Frantz C., Regazzi R.;
"Characterization of granuphlin, a beta cell-specific protein.";
Submitted (SPP-2001) to the EMBL/GenBank/DBJ databases.
EMBL, AF419341; AAL38513.1; -.
InterPro: IPR000008; C2.
InterPro: IPR003315; RPH3A_effector.
PFam: PF00168; C2; 2.
PFam: PF02318; RPH3A_effector; 1.
PRINTS; PR00360; C2DOMAIN.
SMART; SM00239; C2; 2.
PROSITE; PS50004; C2_DOMAIN_2; 2.
SEQUENCE 672 AA: 7590 MW: 6994kDaB5E202400 CRC64;

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DR	PROSITE; PS00343;	GRAM_POS_ANCHORING;	UNKNOWN_1.
DR	PROSITE; PS00012;	PHOSPHOPANTHETHEINE;	UNKNOWN_1.
SQ	SEQUENCE	376 AA;	42761 MW; B1A35979104F5816 CRC64;

Query Match	28.9%;	Score 524.5;	DB 11;	Length 376;
Best Local Similarity	35.1%;	Pred. No. 2.7e-41;		
Matches 124;	Conservative 66;	Mismatches 126;	Indels 37;	Gaps 11;

QY	2	NLPSPASTIPSGFGRHSJSDISTCEKMFQNFQANTGIEFAIHCFTHTSEIOI	61
Pb	40	NLSSSSGHTSLSSAS---GSVMYSVS-----GDFGNLEKVSQVRALDYVESKLEIHFV	91
QY	62	KACKLAVANGEEKKKKCNPVKTYLLPDRSSGCKRRTGVOARNTVDPFOETLKYOVAPO	12
Pb	92	AOCKLAAADAVKCKSDPDKVYKTYLLPDKGCKMKCKTKLVYKTLNPNVYNLTLEKIERGL	15
QY	122	VTRLOVAVMHLGTLARRFYLGSEVITISATWPEEDSTOSFWMHPLPRAKAEKEDSVP--	17
Pb	152	KTORLNLSEVMHNDTFRKNSLGEVBLDETWMDSCKOKMLKYLLKR-----TAPAA	20
QY	180	---OSNGELLYRAKLVFSPRKKLOEADBGDQPSLHGOLCLVLGAKNLPVPRDGTLS	23
Pb	206	LETERRGEM---KTAIDYVP---EPSPGKKLPPT--GEVHTWRECDLPLLRGSHLNS	25
QY	237	FVKGGLTLPD--QOKLRKSPYLKROACEQWKHSFVFGSQTAPALQSSSLHFLVMQALFG	29
Pb	257	FVK--CTILPDSRKROKTRAVGKTTNPVFNHTVYDGFPRDMLAEACELTVMWH--YK	31
QY	296	MNDRLTGGTRIG----SKGDTAVGDAKCSLQWOKVYLSPPNLTMTLTVL	343
Pb	314	LTNOGLGLGRFGTGKSYGEVDMDSSTSEVALWEMKVNPSNNWVEATTEPL	366

```

0Y      62  KAKKILANGEEKKKNKCNVYVYLLIPDDSSOGKKRTGORTVYVTPFOELTKYQVAPAO 121
Db      639  AOCXDLAADVKKQORSDDYVATYLLPDKGKNGKKKTLVYKTLNLPVYNELLRKIKIEOFL 658
0Y      122  VTROLOVSWMHLGLTARRVPLGEVYIISLAWDFEDSTQSFRRHPLRAKAEKEDSV- 179
Db      699  KTORLNTLSVWHRDFFKRNSEFGEVELLEDTWMDPSKONKOLKWPRLRK -----TAPVA 752
0Y      180  --OSNGELTVYKATLVYSPRPRLQOAEQGDOPSLNGOLCLVYLGAKKNLPVRPDGLTNS 236
Db      753  LETERNGM-----KLALOYV-----EESPFGKKLPYT-GEVHIWKECLDLPRLGSHLNS 803
0Y      237  FVKGCLLPD--OQKRLRLKSPYLKQACRPQWKNSEFVSQVTPRAOLQOSLELTYWDAQLF 295
Db      804  FVK--CTILPDRSKRSROKTRAVNGKTBPVFNHTWVYUGFREDMEACVELTWDH--YK 860
0Y      296  MNDRLIGSTRIG-----SKGDTANGSPACSLSKIQOKVYLLSSPMLWTMDLV 343
Db      861  LTNOFLGLGRIGFSTGKSYGTEVYDWMDSITBEVALMEKYNVSPFTWVEATLPL 913

```

OY 2 NIPSSAPSTLIFSGFRHGLSIDSCCTEGNNDNMNVNGEIFAHLHKRTSLSELCI 61
 ||||| :||:: | - | :||| :
Db 587 NLSSSGMTLSLSSA---GSVMYS----GPGNELEVGKSVQFALDYESLKELHFV 630

[illegible]

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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 20 Seconds
(without alignments)
1653.512 Million cell updates/sec

Title: US-09-785-548-2

Perfect score: 1813

Sequence: 1 QNLPSSPAPRTIFSGGFRHG.....QMOKVLSFNLMTDMLVLH 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 283224 seqs, 96134422 residues 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	12.7	511	2	S58399
2	222.5	12.3	441	2	A40707
3	220.5	12.2	439	2	JH0414
4	219	12.1	279	2	S58402
5	218	12.0	537	2	JH0415
6	217.5	12.0	424	2	I51210
7	216.5	11.9	498	2	PC6300
8	215.5	11.9	422	1	BMRT2Y
9	215.5	11.9	422	1	A55417
10	213.5	11.8	386	2	I59387
11	213.5	11.8	400	2	JC2473
12	212	11.7	588	2	A53563
13	211.5	11.7	422	1	BMRT1Y
14	211.5	11.7	422	1	A45486
15	210.5	11.6	427	2	JH0413
16	207	11.4	412	2	JC4921
17	207	11.4	681	2	JX0338
18	207	11.4	684	2	I58166
19	202	11.1	704	2	A48097
20	200.5	11.1	421	2	S09595
21	199.5	11.0	315	2	T32059
22	189.5	10.5	743	2	T00634
23	189.5	10.5	1212	2	T00332
24	188.5	10.4	474	1	BMFSY
25	186	10.3	257	2	T16355
26	186	10.3	403	2	S33318
27	179	9.9	355	2	S58401
28	177.5	9.8	403	2	S58400
29	171	9.4	387	2	JC7398

30	171	9.4	390	2	T28967	hypothetical prote
31	170	9.4	1658	2	T42642	phosphoinositide 3
32	169	9.3	425	2	I59355	synaptotagmin IV -
33	169	9.3	1876	3	T13801	phosphoinositide 3
34	161	8.9	1634	1	JC5500	phosphoinositide 3
35	158.5	8.7	474	2	S68695	B/K protein - rat
36	151	8.3	853	2	T29736	hypothetical prote
37	149	8.2	672	1	KIHUCA	protein kinase C (
38	149	8.2	672	1	KIRTC	protein kinase C (
39	149	8.2	672	1	KIMSCA	protein kinase C (
40	149	8.2	1553	2	T03301	rab3 effector prote
41	149	8.2	1607	2	T21982	hypothetical prote
42	148	8.2	672	1	KIRBC	protein kinase C (
43	148	8.2	1325	2	T25753	hypothetical prote
44	140	7.7	672	1	KIBOC	protein kinase C (
45	139.5	7.7	847	2	A56039	GTPase-activating

ALIGNMENTS

RESULT 1
S58399
cellulotagmin I syti - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S58399
R:Li, C.; Ullrich, B.; Zhang, J.Z.; Anderson, R.G.W.; Brose, N.; Suedhof, T.C.
Nature 375, 594-599, 1995
A:Title: Ca(2+)-dependent and -independent activities of neural and non-neural synapt
A:Reference number: S58399; MUID:95312080; PMID:7791877
A:Accession: S58399
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <LIC>
A:Cross-references: EMBL:U020105; NID:9643653; PIR:AAA87724.1; PID:9643654
C:Superfamily: synaptotagmin; protein kinase C C2 region homology <KC2A>
F:224-337/Domain: protein kinase C C2 region homology <KC2A>
F:336-471/Domain: protein kinase C C2 region homology <KC2B>

Query Match 12.7%; Score 230; DB 2; Length 511;
Best Local Similarity 26.9%; Pred. No. 3.9e-12;
Matches 81; Conservative 57; Mismatches 117; Indels 46; Gaps 13;

QY	38	ANVTGEIEFAHYCKRHSLEICRAKNLAYGEKKKC--NPVVKYTLDPDRSQCK 94	
DB	228	AKSCGKINPSLRDYSEETLIVRIK---AFDLPKACGSSDPYKTYLDPDRKC--K 281	
QY	95	RRTGYQNTVDPFQETLKQVAPQVLRQLOVSVNHLGTARVFLGVIISLATWDF 154	
DB	282	LQTRVHKRTLNFTDENHFVPEYELADRLHLVFDDEFRRHDMIGEVILD-NLFEA 340	
QY	155	EDSTQSEFRWHLRAKAEKYEDSVPSNGELTVRAKVLPSRRKLQEAQEGTDQPSLNG 214	
DB	341	SDLSETSIW---KDIQYATSESVLDGEI-MFSLCYLPTA-----G 377	
QY	215	QCLVYLCAKKNLPVRP-DGTLNSFYKGCGLTPDQQLRLKSPVLRQAC-PQKHSVPS 272	
DB	378	RLLTVIRKRNKAMDITYSDPYKVS-LCDGRRLKRRKTKIKNTLNPNVNEAIIFD 436	
QY	273	GTPPOLROSSLELTVYDQALFGMNDRLGTRLSGKGTAVGADGACSLKLMOKVLSS 332	
DB	437	LPENMDVSLISVMDYDRVGHNE-IIGVCNIGISAE-----GLGRDMNENLAY 466	
QY	333	P 333	
DB	487	P 487	

RESULT 2
A40707
synaptotagmin - Caenorhabditis elegans
N:Alternate names: ric-2

[illegible]

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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 34 Seconds

(without alignments)
419,643 Million cell updates/sec

Title: US-09-785-548-2

Perfect score: 1813
Sequence: 1 QNLPSSPAPSTTFSGGFRHG.....QMKVLSPNMTDMLVLH 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Minimum number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222.5	12.3	441	1	SYT1_CAEEL
2	220.5	12.2	439	1	SY62_DISOM
3	218.5	12.1	432	1	SYT2_MOUSE
4	218	12.0	537	1	SY63_DISOM
5	217.5	12.0	424	1	SYT1_CHICK
6	216.5	11.9	498	1	SYT1_RAT
7	215.5	11.8	422	1	SYT2_RAT
8	214.5	11.8	587	1	SYT3_MOUSE
9	213.5	11.8	386	1	SYT5_RAT
10	212.5	11.7	523	1	SYT5_MOUSE
11	212	11.7	588	1	SYT3_RAT
12	211.5	11.7	421	1	SYT1_MOUSE
13	211.5	11.7	422	1	SYT1_BOVIN
14	211.5	11.7	422	1	SYT1_HUMAN
15	211.5	11.7	590	1	SYT1_HUMAN
16	210.5	11.6	386	1	SYT5_MOUSE
17	210.5	11.6	427	1	SYT5_MOUSE
18	207.5	11.4	386	1	SYT5_HUMAN
19	207	11.4	681	1	RP3A_MOUSE
20	207	11.3	684	1	RP3A_RAT
21	204	11.3	694	1	RP3A_HUMAN
22	202.5	11.2	421	1	SYT1_RAT
23	202.5	11.2	426	1	SY65_APICA
24	202	11.1	704	1	RP3A_BOVIN
25	189.5	10.5	402	1	SYT7_HUMAN
26	188.5	10.4	471	1	SY65_DROME
27	186	10.3	431	1	SYT8_HUMAN
28	186	10.0	430	1	SYT8_MOUSE
29	179	9.9	385	1	SYT8_MOUSE
30	178.5	9.8	403	1	SYT7_MOUSE
31	176.5	9.7	425	1	SYT4_HUMAN
32	176	9.7	430	1	SYT8_RAT
33	169	9.3	425	1	SYT4_RAT

34	164	9.0	425	1	SYT4_MOUSE	P40749 mus musculu
35	161	8.9	1634	1	PK3B_HUMAN	O00750 homo sapien
36	149	8.2	672	1	KPCA_HUMAN	P17252 homo sapien
37	149	8.2	672	1	KPCA_RAT	P05696 rattus norv
38	148	8.2	672	1	KPCA_RABIT	P10102 oryctolagus
39	140	7.7	672	1	KPCA_BOVIN	P04409 bos taurus
40	139.5	7.7	672	1	RS62_RAT	P06373 rattus norv
41	139	7.7	672	1	KPCA_MOUSE	P20444 mus musculu
42	139	7.7	849	1	RS62_HUMAN	Q15283 homo sapien
43	136.5	7.5	1021	1	YP77_CAEEL	P41885 caenorhabdi
44	131	7.2	2083	1	DYSE_MOUSE	O9es47 mus musculu
45	127	7.0	639	1	KPCI_DROME	P05130 drosophila

ALIGNMENTS

RESULT 1
SYT1_CAEEL
ID SYT1_CAEEL STANDARD: PRT: 441 AA.
AC P34693;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Synaptotagmin I.
GN SNT-1 OR F31E8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93313960; PubMed=8391930;
RA Monet M.L., Grundahl K., Meyer B.J., Rand J.B.;
RT "Synaptic function is impaired but not eliminated in C. elegans
Cell 73:1291-1305(1993)."
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
BACKBONE (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
STRUCTURES.
CC -I- TISSUE SPECIFICITY: LOCALIZED TO REGIONS KNOWN TO BE RICH IN
SYNAPSES AND APPEARS TO BE ASSOCIATED WITH SYNAPTIC VESICLES.
CC ALSO FOUND IN SOME NONNEURONAL SECRETORY STRUCTURES.
CC -I- DISEASE: MUTANTS EXHIBIT SEVERE BEHAVIORAL ABNORMALITIES THAT ARE
CHARACTERISTIC OF DEFICIENCIES IN SYNAPTIC FUNCTIONS, INCLUDING
SEVERE LOCOMOTION, FEEDING, AND DEFECTION DEFECTS.
CC -I- SIMILARITY: CONTAINS 2 C2 DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L15302; AAA28145.1; -;
DR EMBL: U55856; AAA98023.1; -;
DR PTR: A40707; A40707.
DR HSSP: P21707; IRSY.
DR WormPep: F31E8.2; CE02711.
DR InterPro: IPR000008; C2.

```

DR InterPro: IPR002149; LRT.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00399; SYNAPTOTAGMIN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00499; C2_DOMAIN_1; 2.
DR PROSITE; PS00004; C2_DOMAIN_2; 2.
KW Transmembrane; Repeat; Synapse; Glycoprotein.
FT DOMAIN 1 69 VESTICULAR (POTENTIAL).
FT TRANSDOM 70 96 POTENTIAL.
FT DOMAIN 97 441 CYTOSOLASMIC (POTENTIAL).
FT TRANSDOM 175 262 C2 DOMAIN 1.
FT DOMAIN 306 397 C2 DOMAIN 2.
SQ SEQUENCE 441 AA; 49904 MM; F8D174337EB472DB CRC64;

Query Match 12.3%; Score 222.5; DB 1; Length 441;
Best Local Similarity 25.9%; Pred. No. 2,6e-12;
Matches 78; Conservative 55; Mismatches 115; Indels 53; Gaps 10;

42 GEIEFAIHYCKRTSHLEICIKACKMAYGEKKKCNPVKYLPLDRSSQGRKRTGYOR 101
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
161 GRIGQKLDYDQGGGLVTVTAQEDLP-GMDMSGSDPYVKIYLLPEKK--KVETKHR 217
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 102 NTVDPTFOETLKQVAPQOLVTRQLOVSVMHLGLTARVFLGEVILISLATWFEDSTQOS 161
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 218 KTLNDFVNEFETLFFKAFNEITAKTLVFAIYDFRFSKHDOIGQVILPLGKID----- 269
QY 162 FRMHDLRKAEYEVSP-----QSGNELTVRAKLVLDSPRKLDEAQEGTDQPSIH 213
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 270 -----LGAVIEKMDIAPPPDDKEAKESKLDGICFSLRV-----PTA- 306
QY 214 GOLCLVLGAKNLPYRPDGLTNS-FVKGCLTLPDQOKLRKSPYLKACQPMKHSFVS 272
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 307 GKLTIVTLEAKNKKMKMDVGLSDPYKIVLMQGGKREKKKTSIKKCTLNPYNNESFSFE 366
QY 273 GVTPAOLKROSSLELTVMQALFGMNDRLTSGRGRSGKSDTVGCGACSLKLNQKVLSS 332
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 367 -VPEQIOIKVSLMTITVMDYDKLGSND-AIGRCLLGCGNCTGA-----ELRHMDMLAS 416
QY 333 P 333
Db 417 P 417

RESULT 2
SY62_DISOM - STANDARD; PRT; 439 AA.
P24506;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Db Synaptotagmin B (Synaptic vesicle protein O-P65-B).
GN P65-B.
OS Discopyge ommata (Electric ray).
OC Eukaryota; Metazoa; Chordata; Ctenista; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squales; Hypnosqualae; Pristiogorae; Batoidae;
OC Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
OX NCBI_TaxId=7785;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE=91273991; Pubmed=2054189;
RA Wendland B., Miller K.G., Schilling J., Scheller R.H.;
RT "Differential expression of the p65 gene family.";
CC Neuron 6:993-1007(1991).
CC -1- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE.
CC -1- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
CC -1- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
CC -1- TISSUE SPECIFICITY: SPINAL CORD, BRAINSTEM, MIDBRAIN AND ELECTRIC

```

CC	ORGAN	-1- SIMILARITY: CONTAINS 2 C2 DOMAINS.	-1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).		
CC	EMBL: M64276; AAA49228.1; -		
DR	PIR: JH0414; JH0414.		
DR	HSSP: p21707; 1BXN.		
DR	InterPro: IPR000008; C2.		
DR	InterPro: IPR002149; LRI.		
DR	InterPro: IPR001565; Synaptotagmin.		
DR	Pfam: PF00168; C2; 2.		
DR	PRINTS: PR00360; C2DOMAIN.		
DR	PRINTS: PR00399; SYNAPTOTAGM.		
DR	SMART: SM00239; C2; 2.		
DR	PROSITE: PS00489; C2_DOMAIN_1; 2.		
DR	PROSITE: PS00004; C2_DOMAIN_2; 2.		
FT	Transmembrane; Repeat; Synapse; Multigene family; Glycoprotein.		
FT	DOMAIN 1	74	74
FT	DOMAIN 1	75	101
FT	DOMAIN 1	102	439
FT	DOMAIN 1	153	399
FT	DOMAIN 1	173	262
FT	DOMAIN 1	304	395
FT	CARBOHYD	6	6
FT	CARBOHYD	46	46
FT	SEQUENCE	439 AA; 49278 MW; 2033505F8DC69F39 CRC64;	
Query Match	12.2%; Score 220.5; DB 1; Length 439;		
Best Local Similarity	26.2%; Pred. No. 3.9e-12;		
Matches 77; Conservative 56; Mismatches 118; Indels 41; Gaps 12;			
QY	42	GELEFAIHQCFKTHSTLEICIKACKNLAVGEERKKKCNPVKTYLLPDRSSQGRKRGVOR	101
DB	161	KIQFSLSDYDFQANOLITVGIQAAELP-ALDMGTSDDPVKVFLLPDKKK-KYETKQVK	217
QY	102	NYVDPTFOELIKQVAPAOVLTRLOVSWMLGTLARKVFLGEVITISLATWPEEDSTTOS	161
DB	218	KTLNLPFNSEFVKVPYQELGKTKLMAVVYDFDRFSKHDGIGQVTVLMLKRVLDGQ--DL	274
QY	162	FWHPLPRAKAEKEDSDYPSQNGELTVRAKLVLPSPRKLEQAEQSTDPDPSLGQCLTVLV	221
DB	275	EMWRDLES-AEKKE---PEKLGIDICTSLRYV-----PTA-GKLVLCIL	312
QY	222	GAKNLPVRPDGTLNS-FVKGCLTLPDQCKLRLKSEVLKQKAC-POWKHSFVSGVTPAOL	279
DB	313	EAKNLLKKMDVGGISDPYKIKHL-LQNGKRLKKKTKYVKNLTPYYNESFSFE-IPFEQI	370
QY	280	ROSSLELTWVDAQLLFGMNDRLIGSTRIGSKCDPAVVGACSLSKLQMKQVLSPP	333
DB	371	QKVQCVTVLDYDKIGKNDAI-----GKTRVGSNASGTELRHMSDMLNP	415
RESULT 3			
ID	SYT2_MOUSE	STANDARD:	PRT; 422 AA.
AC	P46097		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Synaptotagmin II (SYLII).		
GN	SYT2.		
OS	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NC	NCBI_TaxID=10090;		

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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:41:42 ; Search time 197 Seconds
(without alignments)
35.236 Million cell updates/sec

Title: US-09-785-548-2
Perfect score: 1813
Sequence: 1 QNLPSPASTIFSGFRHSG.....QMOKVLSSENLMTDTLVH 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	344	9	US-09-785-548-2
2	1802	99.4	610	9	US-09-785-548-13
3	1802	99.4	610	9	US-09-785-548-43
4	1640	90.5	313	9	US-09-785-548-15
5	1640	90.5	313	9	US-09-785-548-45
6	1234	68.1	363	10	US-09-764-870-393
7	515	28.4	348	10	US-09-764-870-302
8	515	28.4	407	10	US-09-764-870-375
9	430.5	23.7	234	10	US-09-764-870-367
10	234.5	12.9	461	10	US-09-764-870-365
11	208.5	11.5	295	10	US-09-764-870-364
12	194.5	10.7	140	10	US-09-867-550-790
13	186	10.3	179	10	US-09-764-870-360
14	182	10.0	206	10	US-09-764-870-495
15	181.5	10.0	293	10	US-09-935-390A-22
16	174	9.6	1686	12	US-10-092-219-2
17	149	8.2	672	8	US-08-681-219-29
18	148.5	8.2	267	10	US-09-764-870-359
19	140	7.7	208	10	US-09-764-870-497

20	138.5	7.6	836	10	US-09-925-301-1088	Sequence 1088, App
21	136.5	7.5	54	10	US-09-864-761-48954	Sequence 48954, A
22	134	7.4	59	10	US-09-864-761-37895	Sequence 37895, A
23	121	6.7	136	10	US-09-764-870-372	Sequence 372, App
24	118.5	6.5	185	10	US-09-764-870-494	Sequence 494, App
25	113.5	6.3	219	10	US-09-925-300-1448	Sequence 1448, App
26	111.5	6.2	68	10	US-09-864-761-42185	Sequence 42185, A
27	91	5.0	910	10	US-09-935-868-28	Sequence 28, App1
28	88.5	4.9	140	10	US-09-764-870-358	Sequence 358, App
29	87.5	4.8	1193	12	US-10-040-919-2	Sequence 2, App1
30	87	4.8	188	10	US-09-764-870-368	Sequence 368, App
31	87	4.8	299	10	US-09-764-870-388	Sequence 388, App
32	85	4.7	1239	12	US-10-007-805-577	Sequence 577, App
33	84.5	4.7	95	10	US-09-822-635-8	Sequence 8, App1
34	84.5	4.7	95	10	US-09-800-971-10	Sequence 10, App1
35	84.5	4.7	95	10	US-09-927-112-9	Sequence 9, App1
36	84.5	4.7	95	10	US-09-908-664-12	Sequence 12, App1
37	84.5	4.7	95	10	US-09-908-664-21	Sequence 21, App1
38	84	4.6	756	9	US-09-844-988-9	Sequence 9, App1
39	84	4.6	756	10	US-09-796-872-15	Sequence 15, App1
40	84	4.6	756	10	US-09-771-161A-232	Sequence 232, App
41	84	4.6	756	10	US-09-844-908-9	Sequence 9, App1
42	83	4.6	240	9	US-10-114-893-102	Sequence 102, App
43	83	4.6	262	9	US-10-114-893-318	Sequence 318, App
44	82	4.5	507	9	US-10-037-667-3	Sequence 3, App1
45	80.5	4.4	465	10	US-09-969-515-12	Sequence 12, App1

ALIGNMENTS

RESULT 1
US-09-785-548-2
Sequence 2, Appl
Patent No. US2002015577A1
GENERAL INFORMATION:
TITLE OF INVENTION: AVENTIS PHARMACEUTICALS, INC.
FILE REFERENCE: ST00005
CURRENT APPLICATION NUMBER: US/09/785, 548
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-09-785-548-2

Query Match 100.0%; Score 1813; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.9e-177;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QNLPSPASTIFSGFRHSGLSIDSTCTEMGNFNDANVTGEIEFAIHCFKTHSLEIC	60
DB	1	QNLPSPASTIFSGFRHSGLSIDSTCTEMGNFNDANVTGEIEFAIHCFKTHSLEIC	60
QY	61	IRACKNLANGEKKKKCNPKYKTYLLPDRSSOGKRRKGVQNRNTYDPFOETLKKQVAPAQ	120
DB	61	IRACKNLANGEKKKKCNPKYKTYLLPDRSSOGKRRKGVQNRNTYDPFOETLKKQVAPAQ	120
QY	121	LYTRQLOVSWHKGTLARRVFLSVITSLATWPDSTDSFRHNPRAKAEKEDSVQ	180
DB	121	LYTRQLOVSWHKGTLARRVFLSVITSLATWPDSTDSFRHNPRAKAEKEDSVQ	180
QY	181	SNGLTVRAKLVPSRRKLOEAOEGTDPSSLHGQLCLVYGAKNLPVRPDGTLNSFYKG	240
DB	181	SNGLTVRAKLVPSRRKLOEAOEGTDPSSLHGQLCLVYGAKNLPVRPDGTLNSFYKG	240
QY	241	CLTLPDQOKRLKSPVLRKACQMKHSFVSGVTPAOLROSSLETLVWDALFGMDRL	300
DB	241	CLTLPDQOKRLKSPVLRKACQMKHSFVSGVTPAOLROSSLETLVWDALFGMDRL	300

OY 301 LGTRLGSKGDTAVGGDACSLSKLOMOKVLSBNLMTDMLVLH 344
 Db 301 LGTRLGSKGDTAVGGDACSLSKLOMOKVLSBNLMTDMLVLH 344

RESULT 2

US-09-785-548-13
 ; Sequence 13, Application US/09785548
 ; Patent No. US20020155577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
 ; FILE REFERENCE: ST000005
 ; CURRENT APPLICATION NUMBER: US/09/785,548
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 610
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 09-785-548-13

Query Match 99.4%; Score 1802; DB 9; Length 610;
 Best Local Similarity 99.4%; Pred. No. 8.9e-176;
 Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ONLPSPAPSTIFSGFRRHGLSLIDSTCTEMGNPNANVTGEIEFAIHYCFKTHSLEIC 60
 Db 267 ONLPSPAPSTIFSGFRRHGLSLIDSTCTEMGNPNANVTGEIEFAIHYCFKTHSLEIC 326
 OY 61 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRRKTGVQRTNVDPTFOETLKYQVAPAQ 120
 Db 327 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRRKTGVQRTNVDPTFOETLKYQVAPAQ 386
 OY 121 LVTRLOLVSVNHLGLTARVFLGEVIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 180
 Db 387 LVTRLOLVSVNHLGLTARVFLGEVIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 446
 OY 181 SNGELTVAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVLAANKLPVRPDGTLNSFVKG 240
 Db 447 SNGELTVAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVLAANKLPVRPDGTLNSFVKG 506
 OY 241 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTVWDQALFGMNDRL 300
 Db 507 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTVWDQALFGMNDRL 566
 OY 301 LGTRLGSKGDTAVGGDACSLSKLOMOKVLSBNLMTDMLVLH 344
 Db 567 LGTRLGSKGDTAVGGDACSLSKLOMOKVLSBNLMTDMLVLH 610

RESULT 3

US-09-785-548-43
 ; Sequence 43, Application US/09785548
 ; Patent No. US20020155577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
 ; FILE REFERENCE: ST000005
 ; CURRENT APPLICATION NUMBER: US/09/785,548
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 43
 ; LENGTH: 610
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 US-09-785-548-43

Query Match 99.4%; Score 1802; DB 9; Length 610;
 Best Local Similarity 99.4%; Pred. No. 8.9e-176;
 Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ONLPSPAPSTIFSGFRRHGLSLIDSTCTEMGNPNANVTGEIEFAIHYCFKTHSLEIC 60
 Db 267 ONLPSPAPSTIFSGFRRHGLSLIDSTCTEMGNPNANVTGEIEFAIHYCFKTHSLEIC 326
 OY 61 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRRKTGVQRTNVDPTFOETLKYQVAPAQ 120
 Db 327 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRRKTGVQRTNVDPTFOETLKYQVAPAQ 386
 OY 121 LVTRLOLVSVNHLGLTARVFLGEVIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 180
 Db 387 LVTRLOLVSVNHLGLTARVFLGEVIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 446
 OY 181 SNGELTVAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVLAANKLPVRPDGTLNSFVKG 240
 Db 447 SNGELTVAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVLAANKLPVRPDGTLNSFVKG 506
 OY 241 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTVWDQALFGMNDRL 300
 Db 507 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLELTVWDQALFGMNDRL 566
 OY 301 LGTRLGSKGDTAVGGDACSLSKLOMOKVLSBNLMTDMLVLH 344
 Db 567 LGTRLGSKGDTAVGGDACSLSKLOMOKVLSBNLMTDMLVLH 610

RESULT 4

US-09-785-548-15
 ; Sequence 15, Application US/09785548
 ; Patent No. US20020155577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF P
 ; FILE REFERENCE: ST000005
 ; CURRENT APPLICATION NUMBER: US/09/785,548
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 313
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 US-09-785-548-15

Query Match 90.5%; Score 1640; DB 9; Length 313;
 Best Local Similarity 99.4%; Pred. No. 1.2e-159;
 Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 32 MGNPDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAYGEEKKKKCNPYKTYLLPDRSS 91
 Db 1 MGNPDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAYGEEKKKKCNPYKTYLLPDRSS 60
 OY 92 QGKRRKTGVQRTNVDPTFOETLKYQVAPAOVLTRLOLVSVNHLGLTARVFLGEVIISLAT 151
 Db 61 QGKRRKTGVQRTNVDPTFOETLKYQVAPAOVLTRLOLVSVNHLGLTARVFLGEVIISLAT 120
 OY 152 WDFEDSTQSRFMRHLRAKAEKEDSVPOSNGLTVAKLVLPSPRKLQEAQEGTDQPS 211
 Db 121 WDFEDSTQSRFMRHLRAKAEKEDSVPOSNGLTVAKLVLPSPRKLQEAQEGTDQPS 180
 OY 212 LHGOLCLVLAANKLPVRPDGTLNSFVKGCLTLPDQOKLRLKSPVLRKQACPOWKHSFV 271
 Db 181 LHGOLCLVLAANKLPVRPDGTLNSFVKGCLTLPDQOKLRLKSPVLRKQACPOWKHSFV 240
 OY 272 SGVTPAOLROSSLELTVWDQALFGMNDRLGTRLGSKGDTAVGGDACSLSKLOMOKVLS 331
 Db 241 SGVTPAOLROSSLELTVWDQALFGMNDRLGTRLGSKGDTAVGGDACSLSKLOMOKVLS 300
 OY 332 SPNLMTDMLVLH 344
 Db 301 SPNLMTDMLVLH 313

RESULT 5
US-09-785-548-45
Sequence 45, Application US/09785548
Patent No. US20020155577A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
FILE REFERENCE: ST00005
CURRENT APPLICATION NUMBER: US/09/785,548
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-785-548-45

Query Match
Best Local Similarity 90.5%; Score 1640; DB 9; Length 313;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 32 MGNFMANVTGEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 91
1 MGNFMANVTGEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 60
QY 92 GCKRKTGVQNTVDPFQETLKYQVAPAOQVTRLOLQVSVHGLTARVFLGEVYISLAT 151
61 GCKRKTGVQNTVDPFQETLKYQVAPAOQVTRLOLQVSVHGLTARVFLGEVYISLAT 120
QY 152 WPEEDSTQSFRRHPLRAKAEKEDSVOSNGELTVRAKLVLSRPRKLOAOGSTOOPS 211
121 WPEEDSTQSFRRHPLRAKAEKEDSVOSNGELTVRAKLVLSRPRKLOAOGSTOOPS 180
DB 212 LHGQCLVLYGAKNLPVRPBDGLNSEFVGCLTLPDQOKLRKSEVLRKQACPQKHSFEV 271
181 LHGQCLVLYGAKNLPVRPBDGLNSEFVGCLTLPDQOKLRKSEVLRKQACPQKHSFEV 240
QY 272 SSVTPAQLQSSLELTVMDALFGMDRLIGSTRGSGGTAVGGDCSLKLOMOKVLS 331
241 SSVTPAQLQSSLELTVMDALFGMDRLIGSTRGSGGTAVGGDCSLKLOMOKVLS 300
DB 332 SPNLTMDTLVLH 344
301 SPNLTMDTLVLH 313
QY 301 SPNLTMDTLVLH 313

RESULT 6
US-09-764-870-393
Sequence 393, Application US/09764870
Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 393
LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (29)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (294)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (312)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (316)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (323)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (335)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-870-393

Query Match
Best Local Similarity 68.1%; Score 1234; DB 10; Length 363;
Matches 234; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ONLPSPAPSTIFSGFRGSLISDSTCTEMGNFMANVTGEIEFAIHCFKTHSLEIC 60
DB 124 ONLPSPAPSTIFSGFRGSLISDSTCTEMGNFMANVTGEIEFAIHCFKTHSLEIC 183
QY 61 IKACKNLAYGEEKKKCNPYKTYLLPDRSSOQKRTGVQNTVDPFQETLKYQVAPQ 120
DB 184 IKACKNLAYGEEKKKCNPYKTYLLPDRSSOQKRTGVQNTVDPFQETLKYQVAPQ 243
QY 121 LVTRLOQVSVHGLTARVFLGEVYISLATWDEEDSTQSFRRHPLRAKAEKEDSVQ 180
DB 244 LVTRLOQVSVHGLTARVFLGEVYISLATWDEEDSTQSFRRHPLRAKAEKEDSVQ 303
QY 181 SNGELTVRAKLVLSRPRKLOAOGSTOOPS LHGQCLVLYGAKNLPVRPBDGLNSEFVG 240
DB 304 SNGELTVRAKLVLSRPRKLOAOGSTOOPS LHGQCLVLYGAKNLPVRPBDGLNSEFVG 363

RESULT 7
US-09-764-870-502
Sequence 502, Application US/09764870
Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 502
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-870-502

Query Match
Best Local Similarity 28.4%; Score 515; DB 10; Length 348;
Matches 120; Conservative 62; Mismatches 119; Indels 34; Gaps 10;

QY 20 GSLISDSTCTEMGNFMANVTGEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCN 79
DB 27 GSVMSVYS-----GDEGNLEVKGNIDQFALEYVSLKELHVFVQCKDLAADVKKQSDP 81
QY 80 YKTYLLPDRSSOQKRTGVQNTVDPFQETLKYQVAPAOQVTRLOLQVSVHGLTAR 139
DB 82 YKATYLLPDRSSOQKRTGVQNTVDPFQETLKYQVAPAOQVTRLOLQVSVHGLTAR 141

[illegible]

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      : FILE REFERENCE: PT14
      : CURRENT APPLICATION NUMBER: US/09/764,870
      : CURRENT FILING DATE: 2001-01-17
      : Prior application data removed - consult PALM or file wrapper
      : NUMBER OF SEQ ID NOS: 646
      : SOFTWARE: PatentIn Ver. 2.0
      : SEQ ID NO 367
      : LENGTH: 234
      : TYPE: PRT
      : ORGANISM: Homo sapiens
US-09-764-870-367

Query Match          23.7%; Score 430.5; DB 10; Length 234;
Best Local Similarity 41.4%; Pred.No.2.7e-36;
Matches   98; Conservative    37; Mismatches   89; Indels    19; Gaps       7

QY      62 KACKLALAGEKKKCNPNRYKYTYLLPDDSSGCKRTGVGNRVNDYPFOETLKYYAAPQL 121
        : | | | | : | | : | | | | | | | | | | | | | | | | | | | : |
DB      2 RECHOLAVADEKCKSNRPYKYTYLLPDDKSROCKRTSTIKRDVNPYDTELTLEYIEPSLL 61

QY     122 VTROLQAVSWHLGTARAREFLGEIVILISLATWDFEDSTQSFRMHPLRAK-AKEYEDSVQ 180
        : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      62 AORTLOEFSVMHNGRGGRNTFLGEALIDMSWLDKKDHLCL--PLHGKISAESPTGLPS 118

QY      181 SNGELTVFAKLVLPSR-----PRKIQEAOGESTDPPSLHSQCLOCVLVIAGKNL-PVRPDGTL 234
        : | | | | : | | : | | : | | : | | : | | : | | : | |
DB     119 HKGELVASIKIYPAKRTFVGGDGRKSKSGEG-----GELQVMIKEAKNLTAAAGA GTS 171

QY     235 NSPYFGCTLPDPQOL-RUKSPVEKIOACPOMKSHSFVSQVPAQLROSSELTLYWD 290
        : | | | | | | | : | | : | | | | : | | : | | | | | | | | | |
DB     172 DSFYKGYL-LPRRNKASKRKITPVMMKTLNPHYNHTFTVINGVLEDDIQHMCELTLYWD 227

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RESULT 10
US-09-764-870-365
/ Sequence 365, Application US/09764870
/ Patent No. US20020042386A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT214
/ CURRENT APPLICATION NUMBER: US/09/764,870
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 646
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 365
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-764-870-365

Query Match          12.9%  Score 234.5;  DB 10;  Length 461;
Best Local Similarity 27.2%  Pred. No. 7.4e-16;
Matches 91;  Conservative 60;  Mismatches 155;  Indels 49;  Gaps 15;

QY      4  PSSAPSTIFSGGRRHGLSIDSTCTMGNFNDANVTGELFAHYCFKTHSLSTICA 63
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      147 PAAQOPTSI---GRKPELYKQKSVSDGDAKSEATKSGKINFSLRXYETETLLIVRIIK 203
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      64 CKNLVAGEKKKK---NPVYKTYLLPDRSSQGRKKGTQVORTNTPPQETLKQVAPAQ 120
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      204 ----AFDLPAKDFGSSDPYKITYLLPDKRC-KIQTVAHRTLTNPPTDENHFVPEE 257
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      121 LVTRQLOVSVHNLGTLARVYLGVEYIISLATWDEFDSTQSFRRMHPRAKAEKYEDSVQ 180
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      258 LADKKLHLSVDPDRFRSHMDIGEVIID-NLEFASDLSRETSIN-----KDIQVATSESV 311
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      181 SNGELTVRAKLVLPSSRPKRIQEAQEGTDQPSLHGQALVVLGAKNLPVPR-DGTLSNFEVK 239
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      312 DLGRI-MFSLCYLPTA-----GRLLTLTVKCRNLKAMDITGYSDEPYK 353
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      240 GCLTLPRDQKIRLKSPLYLRKQAC-PQWKHSFVSFGVTPAQLRQSSLELTWVDQALEGMD 298

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GenCore version 5.1.3
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OM protein - protein search, using sw model

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Title: US-09-785-548-2
Sequence: 1 QNLPSSPAPSTIFSGFRHG.....QMOKVLSPPNMTDITLVIH 344

Scoring table: BLOSUM62
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Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

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1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211.5	11.7	422	3	US-08-872-979-8
2	179	9.9	355	3	US-08-872-979-7
3	176.5	9.7	425	4	US-09-036-315-2
4	174	9.6	1686	4	US-09-355-160D-2
5	173	9.5	375	3	US-08-872-979-3
6	170	9.4	137	2	US-08-609-049A-15
7	170	9.4	137	4	US-09-170-996-15
8	170	9.4	1658	2	US-08-609-049A-13
9	170	9.4	1658	4	US-09-170-996-13
10	170	9.4	1726	2	US-08-609-049A-30
11	170	9.4	1726	4	US-09-170-996-30
12	169	9.3	137	2	US-08-609-049A-14
13	169	9.3	137	4	US-09-170-996-14
14	169	9.3	425	4	US-09-036-315-5
15	169	9.3	1876	2	US-08-609-049A-12
16	169	9.3	1876	4	US-08-609-049A-28
17	169	9.3	1876	4	US-09-170-996-12
18	169	9.3	1876	4	US-09-170-996-38
19	135.5	7.5	113	4	US-09-036-315-10
20	132	7.3	140	2	US-08-609-049A-16
21	132	7.3	140	4	US-09-170-996-16
22	128.5	7.1	120	4	US-09-036-315-9
23	122	6.7	117	4	US-09-036-315-6
24	120	6.6	136	4	US-08-609-049A-18
25	120	6.6	136	2	US-09-170-996-18
26	120	6.6	138	2	US-08-609-049A-17
27	120	6.6	138	4	US-09-170-996-17

28	120	6.6	671	6	5266464-2
29	117.5	6.5	115	4	US-09-036-315-8
30	86	4.7	1148	2	US-08-313-185-58
31	86	4.7	1148	3	US-09-082-614A-58
32	84	4.6	756	4	US-08-887-518-4
33	84	4.6	756	2	US-09-023-321-4
34	84	4.6	756	2	US-08-890-853-2
35	84	4.6	756	2	US-09-032-475-4
36	84	4.6	756	2	US-09-099-125A-2
37	84	4.6	756	2	US-09-099-124A-2
38	84	4.6	756	4	US-09-032-476-2
39	84	4.6	756	4	US-08-890-854-2
40	84	4.6	756	4	US-09-023-324-2
41	84	4.6	756	4	US-09-168-629-15
42	84	4.6	756	4	US-08-910-820-9
43	83.5	4.6	1019	1	US-08-271-364A-7
44	83.5	4.6	1019	2	US-08-222-715B-26
45	83	4.6	240	2	US-08-738-367-7

ALIGNMENTS

```
RESULT 1
US-08-872-979-8
; Sequence 8, Application US/08872979
; Patent No. 6074844
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,979
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0320 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 338658
; US-08-872-979-8

Query Match 11.7%; Score 211.5; DB 3; Length 422;
Best Local Similarity 25.5%; Pred. No. 5,2e-15;
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